



1

SEQUENCE LISTING

<110> LOSORDO, DOUGLAS W.
KISHORE, RAJ

<120> CELL MODULATION USING A CYTOSKELETAL PROTEIN

<130> 58098 (71417)

<140>

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<150> 60/400,084

<151> 2002-08-01

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 586

<212> PRT

<213> Homo sapiens

<400> 1

Met Pro Lys Pro Ile Asn Val Arg Val Thr Thr Met Asp Ala Glu Leu
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Glu Phe Ala Ile Gln Pro Asn Thr Thr Gly Lys Gln Leu Phe Asp Gln
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Val Val Lys Thr Ile Gly Leu Arg Glu Val Trp Tyr Phe Gly Leu His
35 40 45
Tyr Val Asp Asn Lys Gly Phe Pro Thr Trp Leu Lys Leu Asp Lys Lys
50 55 60
Val Ser Ala Gln Glu Val Arg Lys Glu Asn Pro Leu Gln Phe Lys Phe
65 70 75 80
Arg Ala Lys Phe Tyr Pro Glu Asp Val Ala Glu Glu Leu Ile Gln Asp
85 90 95
Ile Thr Gln Lys Leu Phe Phe Leu Gln Val Lys Glu Gly Ile Leu Ser
100 105 110
Asp Glu Ile Tyr Cys Pro Pro Glu Thr Ala Val Leu Leu Gly Ser Tyr
115 120 125
Ala Val Gln Ala Lys Phe Gly Asp Tyr Asn Lys Glu Val His Lys Ser
130 135 140
Gly Tyr Leu Ser Ser Glu Arg Leu Ile Pro Gln Arg Val Met Asp Gln
145 150 155 160
His Lys Leu Thr Arg Asp Gln Trp Glu Asp Arg Ile Gln Val Trp His
165 170 175

Ala	Glu	His	Arg	Gly	Met	Leu	Lys	Asp	Asn	Ala	Met	Leu	Glu	Tyr	Leu	180	185	190
Lys	Ile	Ala	Gln	Asp	Leu	Glu	Met	Tyr	Gly	Ile	Asn	Tyr	Phe	Glu	Ile	195	200	205
Lys	Asn	Lys	Lys	Gly	Thr	Asp	Leu	Trp	Leu	Gly	Val	Asp	Ala	Leu	Gly	210	215	220
Leu	Asn	Ile	Tyr	Glu	Lys	Asp	Asp	Lys	Leu	Thr	Pro	Lys	Ile	Gly	Phe	225	230	235
Pro	Trp	Ser	Glu	Ile	Arg	Asn	Ile	Ser	Phe	Asn	Asp	Lys	Lys	Phe	Val	245	250	255
Ile	Lys	Pro	Ile	Asp	Lys	Lys	Ala	Pro	Asp	Phe	Val	Phe	Tyr	Ala	Pro	260	265	270
Arg	Leu	Arg	Ile	Asn	Lys	Arg	Ile	Leu	Gln	Leu	Cys	Met	Gly	Asn	His	275	280	285
Glu	Leu	Tyr	Met	Arg	Arg	Arg	Lys	Pro	Asp	Thr	Ile	Glu	Val	Gln	Gln	290	295	300
Met	Lys	Ala	Gln	Ala	Arg	Glu	Glu	Lys	His	Gln	Lys	Gln	Leu	Glu	Arg	305	310	315
Gln	Gln	Leu	Glu	Thr	Glu	Lys	Lys	Arg	Arg	Glu	Thr	Val	Glu	Arg	Glu	325	330	335
Lys	Glu	Gln	Met	Met	Arg	Glu	Lys	Glu	Glu	Leu	Met	Leu	Arg	Leu	Gln	340	345	350
Asp	Tyr	Glu	Glu	Lys	Thr	Lys	Lys	Ala	Glu	Arg	Glu	Leu	Ser	Glu	Gln	355	360	365
Ile	Gln	Arg	Ala	Leu	Gln	Leu	Glu	Glu	Glu	Arg	Lys	Arg	Ala	Gln	Glu	370	375	380
Glu	Ala	Glu	Arg	Leu	Glu	Ala	Asp	Arg	Met	Ala	Ala	Leu	Arg	Ala	Lys	385	390	395
Glu	Glu	Leu	Glu	Arg	Gln	Ala	Val	Asp	Gln	Ile	Lys	Ser	Gln	Glu	Gln	405	410	415
Leu	Ala	Ala	Glu	Leu	Ala	Glu	Tyr	Thr	Ala	Lys	Ile	Ala	Leu	Leu	Glu	420	425	430
Glu	Ala	Arg	Arg	Arg	Lys	Glu	Asp	Glu	Val	Glu	Glu	Trp	Gln	His	Arg	435	440	445
Ala	Lys	Glu	Ala	Gln	Asp	Asp	Leu	Val	Lys	Thr	Lys	Glu	Glu	Leu	His	450	455	460
Leu	Val	Met	Thr	Ala	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Val	Tyr	Glu	Pro	465	470	475
																		480

Val Ser Tyr His Val Gln Glu Ser Leu Gln Asp Glu Gly Ala Glu Pro
485 490 495

Thr Gly Tyr Ser Ala Glu Leu Ser Ser Glu Gly Ile Arg Asp Asp Arg
500 505 510

Asn Glu Glu Lys Arg Ile Thr Glu Ala Glu Lys Asn Glu Arg Val Gln
515 520 525

Arg Gln Leu Val Thr Leu Ser Ser Glu Leu Ser Gln Ala Arg Asp Glu
530 535 540

Asn Lys Arg Thr His Asn Asp Ile Ile His Asn Glu Asn Met Arg Gln
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Gly Arg Asp Lys Tyr Lys Thr Leu Arg Gln Ile Arg Gln Gly Asn Thr
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Lys Gln Arg Ile Asp Glu Phe Glu Ala Leu
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atactgtccc tgca

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